

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: March 1, 2001, 16:08:56 ; Search time 299.73 Seconds
(without alignments)
17.597 Million cell updates/sec

Title: US-09-331-631a-1_COPY_29_73
Perfect score: 252
Sequence: 1 SEPDROEYECCKRCQMOLFT.....RCVSQCKRFEEDIDMSKYD 45

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 374700 seqs, 117207915 residues

Total number of hits satisfying chosen parameters: 374700

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 10%
Listing first 45 summaries

Database :
1: SPTRMBL_15:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mammal:*
8: sp_mhc:*
9: sp_organelle:*
10: sp_phase:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
15: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Length	DB ID	Description
1	252	100.0	666 10 Q9SP15	Q9SP15 macadamia 1
2	252	100.0	666 10 Q9SP14	Q9SP14 macadamia 1
3	180	71.4	625 10 Q9SP13	Q9SP13 macadamia 1
4	70.5	28.0	525 10 Q43358	Q43358 theobroma c
5	70.5	28.0	593 10 Q9SEW4	Q9SEW4 juglans reg
6	67	26.6	810 10 Q9ZWT3	Q9ZWT3 cucurbita m
7	67	26.6	1170 6 Q28179	Q28179 bos taurus
8	65	25.8	393 10 Q9ZTP0	Q9ZTP0 oryza sativ
9	64	25.4	554 10 Q9SG14	Q9SG14 arabidopsis
10	63	25.0	564 6 Q9TTS4	Q9TTS4 bos taurus
11	62.5	24.8	489 10 Q9SP11	Q9SP11 glycine max
12	62	24.6	875 4 Q60278	Q60278 homo sapien
13	62	24.6	941 4 Q9UKT2	Q9UKT2 homo sapien
14	62	24.6	941 4 Q9UHF8	Q9UHF8 homo sapien
15	62	24.6	941 4 Q9NZ08	Q9NZ08 homo sapien
16	62	24.6	1947 2 Q9RFK7	Q9RFK7 stigmatella
17	61	24.2	554 10 P93719	P93719 petunia hyb
18	61	24.2	930 11 Q9J123	Q9J123 ratius norv
19	59.5	23.6	92 5 Q9VTN3	Q9VTN3 drosophila

20	59.5	23.6	3078 5 Q26031	Q26031 plasmodium
21	59.5	23.6	3696 5 Q9N4B9	Q9N4B9 caenorhabdi
22	59	23.4	387 10 Q9S901	Q9S901 arabidopsis
23	58	23.0	242 5 Q19919	Q19919 caenorhabdi
24	58	23.0	489 5 Q61650	Q61650 drosophila
25	58	23.0	490 5 Q9VFN5	Q9VFN5 drosophila
26	58	23.0	1421 10 Q49539	Q49539 arabidopsis
27	57.5	22.8	364 10 Q9LIR8	Q9LIR8 arabidopsis
28	57	22.6	316 5 Q96288	Q96288 plasmodium
29	57	22.6	725 12 Q9JF74	Q9JF74 vaccinia vl
30	55.5	22.0	205 5 Q9VTA7	Q9VTA7 drosophila
31	55	21.8	348 5 Q96290	Q96290 plasmodium
32	55	21.8	402 10 Q9ZRH8	Q9ZRH8 oryza sativ
33	55	21.8	623 10 Q9SU72	Q9SU72 arabidopsis
34	55	21.8	822 5 Q00901	Q00901 leishmania
35	55	21.8	4123 4 Q75851	Q75851 homo sapien
36	54.5	21.6	381 5 Q9VTP5	Q9VTP5 drosophila
37	54.5	21.6	1259 5 Q44971	Q44971 caenorhabdi
38	54.5	21.6	2703 5 Q9VEG7	Q9VEG7 drosophila
39	54.5	21.6	2715 5 Q61603	Q61603 drosophila
40	54	21.4	314 10 Q40489	Q40489 nicotiana t
41	54	21.4	607 10 Q9MA04	Q9MA04 arabidopsis
42	54	21.4	880 1 Q9U2C8	Q9U2C8 pyrococcus
43	53.5	21.2	67 5 Q18132	Q18132 caenorhabdi
44	53.5	21.2	450 4 Q75595	Q75595 homo sapien
45	53.5	21.2	450 4 Q9UNA8	Q9UNA8 homo sapien

ALIGNMENTS

RESULT 1				
Q9SP15		PRELIMINARY;	PRT;	666 AA.
ID Q9SP15				
AC Q9SP15				
DT 01-MAY-2000 (TREMBLrel. 13, Created)				
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				
DT 01-OCT-2000 (TREMBLrel. 15, Last annotation update)				
DE VICILIN PRECURSOR.				
GN AMP2.				
OS Macadamia integrifolia (Macadamia nut).				
OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;				
OC Magnoliophyta; Eudicotyledons; Proteaceae; Macadamia.				
OX NCBI_TaxID=60698;				
RN [1]				
RP SEQUENCE FROM N.A.				
RC TISSUE=NUT KERNEL;				
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.;				
RT "A family of antimicrobial peptides is produced by processing of a 7S				
RT globulin protein in Macadamia integrifolia kernels.";				
RL Plant J. 0:0-0(1999).				
DR EMBL; AF161883; AAD54244.1; -				
DR HSSP; P02853; 2PHL.				
DR INTERPRO; IPR001113; -				
DR PFM; PF00546; Seedstore_7s; 1.				
DR SEQUENCE 666 AA; 78217 MW; C752B884B2DF0224 CRC64;				
SO				
Query Match	100.0%;	Score 252;	DB 10;	Length 666;
Best Local Similarity	100.0%;	Pred. No. 5;	9e-24;	
Matches 45;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
OY 1 SEPDROEYECCKRCQMOLFTSGMRCVSQCKRFEEDIDMSKYD 45				
Db 29 SEPDROEYECCKRCQMOLFTSGMRCVSQCKRFEEDIDMSKYD 73				
RESULT 2				
ID Q9SP14		PRELIMINARY;	PRT;	666 AA.
AC Q9SP14				
DT 01-MAY-2000 (TREMBLrel. 13, Created)				
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)				

DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE VICILIN PRECURSOR.
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: Proteaceae: Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NOT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.:
RT "A family of antimicrobial peptides is produced by processing of a 7S
globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL: AF161884; AAD54245.1; -.
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
SQ SEQUENCE 666 AA; 78243 MW; 0ECA22F8710F8A7B CRC64;

Query Match 100.0%; Score 252; DB 10; Length 666;
Best Local Similarity 100.0%; Pred. No. 5.9e-24;
Matches 45; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 SEPDROEYECCKRCQMOLSTSGQMRRCVSQCDKRFEDIDMSKYD 45
DB 29 SEPDROEYECCKRCQMOLSTSGQMRRCVSQCDKRFEDIDMSKYD 73

RESULT 3
OQSP3 ID OQSP3; PRELIMINARY; PRT; 625 AA.
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE VICILIN PRECURSOR (FRAGMENT).
GN AMP2.
OS Macadamia integrifolia (Macadamia nut).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: Proteaceae: Macadamia.
OX NCBI_TaxID=60698;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=NOT KERNEL;
RA Marcus J.P., Goulter K.C., Green J.L., Manners J.M.:
RT "A family of antimicrobial peptides is produced by processing of a 7S
globulin protein in Macadamia integrifolia.";
RL Plant J. 0:0-0(1999).
DR EMBL: AF161885; AAD54246.1; -.
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
FT NON_TER 1 1
SQ SEQUENCE 625 AA; 73586 MW; 415808A89D370296 CRC64;

Query Match 71.4%; Score 180; DB 10; Length 625;
Best Local Similarity 100.0%; Pred. No. 6.8e-15;
Matches 32; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 14 QCMOLSTSGQMRRCVSQCDKRFEDIDMSKYD 45
DB 1 QCMOLSTSGQMRRCVSQCDKRFEDIDMSKYD 32

RESULT 4
ID 043358 PRELIMINARY; PRT; 525 AA.
AC 043358;
DT 01-NOV-1996 (Tremblrel. 01, Created)
DT 01-NOV-1996 (Tremblrel. 01, Last sequence update)

DT 01-OCT-2000 (Tremblrel. 15, last annotation update)
DE VICILIN PRECURSOR.
GN CSV.
OS Theobroma cacao (Cacao).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eustosids II;
OC Malvales: Malvaceae: Theobroma.
OX NCBI_TaxID=3641;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=LEAVES;
RX MEDLINE=92286309; PubMed=1600151;
RA Moehentz L., Fritz P.J.:
RT "Comparison of the structure and nucleotide sequences of vicilin genes
of cocoa and cotton raise questions about vicilin evolution.";
RL Plant Mol. Biol. 18:1173-1176(1992).
DR EMBL: X62625; CAA44493.1; -.
DR EMBL: X62626; CAA44494.1; -.
DR HSSP: P02853; 2PHL.
DR MENDEL: 30919; Thecc:1188;30919.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
DR PRODOM: PD081059; -. 1.
KW Signal.
FT SIGNAL 1 24 POTENTIAL.
FT CHAIN 25 525 VICILIN.
SQ SEQUENCE 525 AA; 60798 MW; 19114CD5C248905D CRC64;

Query Match 28.0%; Score 70.5; DB 10; Length 525;
Best Local Similarity 32.4%; Pred. No. 0.39;
Matches 11; Conservative 11; Mismatches 11; Indels 1; Gaps 1;

OY 5 ROEYECCKRCQMOLSTSGQMRRCVSQCDKRFEE 37
DB 39 ROEYECCKRCQMOLSTSGQMRRCVSQCDKRFEE 72

RESULT 5
OQSE4 ID OQSE4; PRELIMINARY; PRT; 593 AA.
AC OQSE4;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE VICILIN-LIKE PROTEIN PRECURSOR (FRAGMENT).
OS Juglans regia (English walnut).
OC Eukaryota: Viridiplantae: Embryophyta: Tracheophyta: Spermatophyta:
OC Magnoliophyta: eudicotyledons: core eudicots: Rosidae: eustosids I;
OX NCBI_TaxID=51240;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=CV. SUNLAND; TISSUE=SOMATIC EMBRYO LINE;
RA Teuber S.S., Jarvis K.C., Peterson W.R., Danekar A.M., Ansari A.A.:
RT "Identification and cloning of a cDNA encoding a vicilin-like protein,
Jug r 2, from English walnut kernel (Juglans regia): a major food
allergen.";
RL Submitted (MAY-1998) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF066055; AAF18269.1; -.
DR HSSP: P02853; 2PHL.
DR INTERPRO: IPR001113; -.
DR PFAM: PF00546; Seedstore_7s; 1.
FT NON_TER 1 1
SQ SEQUENCE 593 AA; 69990 MW; 9BA127E19B18C0D8 CRC64;

Query Match 28.0%; Score 70.5; DB 10; Length 593;
Best Local Similarity 29.4%; Pred. No. 0.44;
Matches 10; Conservative 15; Mismatches 8; Indels 1; Gaps 1;
OY 5 ROEYECCKRCQMOLSTSGQMRRCVSQCDKRFEE 37
DB 11 ROEYECCKRCQMOLSTSGQMRRCVSQCDKRFEE 72

Db 120 Q00YHRCRCRCQIDBSPERORCCQRCEROYKE 153

RESULT 6

ID 092WT13 PRELIMINARY; PRT; 810 AA.

AC 092WT13;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE PV100.

OS Cucurbita maxima (Pumpkin) (Winter squash).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;

OC Cucurbitales; Cucurbitaceae; Cucurbita.

OX NCBI_Taxid=3661;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-KUKOKAWA AMAKURI NANKIN; TISSUE-COTYLEDON;

RX MEDLINE=99107919; PubMed=9891029;

RA Yamada K., Shimada T., Kondo M., Nishimura M., Hara-Nishimura I.;

RT "Multiple functional proteins are produced by cleaving Asn-Gln bonds

RL J. Biol. Chem. 274:2563-2570(1999).

DR EMBL; AB019195; BAA34056.1; -.

DR HSSP; P02853; 2PHL.

DR INTERPRO; IPR001113; -.

DR PFAM; PF00546; Seedstore_7s; 1.

DR PRODOM; PD081059; -; 1

SO SEQUENCE 810 AA; 97314 MW; A829A3F7542266AB CRC64;

Query Match 26.6%; Score 67; DB 10; Length 810;

Best Local Similarity 34.1%; Pred. No. 1.6;

Matches 15; Conservative 6; Mismatches 15; Indels 8; Gaps 2;

OY 5 ROYEBCRCQCMQLETS-GQMRRCVSCDKRFE-----EDID 40

Db 75 RAEYEVCLRCQVAREGVEQCRKEQCEERLREREGRGEDVD 118

RESULT 7

ID 028179 PRELIMINARY; PRT; 1170 AA.

AC 028179;

DT 01-NOV-1996 (TREMBlrel. 01, Created)

DT 01-NOV-1998 (TREMBlrel. 08, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE THROMBOSPONDIN 1.

GN TSP-1.

OS Bos taurus (Bovine).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;

OC Bovidae; Bovinae; Bos.

OX NCBI_Taxid=9913;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-HOLSTEIN; TISSUE-ANTERIOR TOOTH;

RX MEDLINE=98173773; PubMed=9507054;

RA Ueno A., Yamashita K., Nagata T., Tsurumi C., Miwa Y., Kitamura S.,

RA Inoue H.;

RT "cDNA cloning of bovine thrombospondin 1 and its expression in

RL odontoblasts and predentin."

RL Blochim. Biophys. Acta 1382:17-22(1998).

RN [2]

RP SEQUENCE OF 1-18 FROM N.A.

RC TISSUE-AORTIC ENDOTHELIUM;

RA Zafar R.S., Moll Y.D., Womack J.F., Walz D.A.;

RL Submitted (MAY-1995) to the EMBL/GenBank/DBJ databases.

DR EMBL; X87619; CAA60951.1; -.

DR HSSP; P35555; 1BMN.

DR INTERPRO; IPR000561; -.

DR INTERPRO; IPR000884; -.

DR INTERPRO; IPR001007; -.

DR INTERPRO; IPR001791; -.

DR INTERPRO; IPR001881; -.

DR INTERPRO; IPR002465; -.

DR INTERPRO; IPR003129; -.

DR PFAM; PF00008; EGF; 2.

DR PFAM; PF00090; TSP_1/ 3.

DR PFAM; PF00093; WVC; 1.

DR PFAM; PF02210; TSPN; 1.

DR PROSITE; PS00340; RECEPTOR_CYTOKINES_2; UNKNOWN_2.

DR PROSITE; PS01186; EGF_2; 1.

DR PROSITE; PS01208; WVC; 1.

SO SEQUENCE 1170 AA; 129533 MW; 0DD6ADF3E5FA031A CRC64;

Query Match 26.6%; Score 67; DB 6; Length 1170;

Best Local Similarity 39.5%; Pred. No. 2.3;

Matches 15; Conservative 6; Mismatches 11; Indels 6; Gaps 2;

OY 13 RQCMQLE----TSQMRRC-VSCDKRFEEDIDMSKY 44

Db 404 RSCDSLNNRCGSSVQTRTCHIQCDKRFKODGGMSHW 441

RESULT 8

ID 092TP0 PRELIMINARY; PRT; 393 AA.

AC 092TP0;

DT 01-MAY-1999 (TREMBlrel. 10, Created)

DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)

DT 01-MAY-1999 (TREMBlrel. 10, Last annotation update)

DE HYPOTHEORETICAL 45.3 KDA PROTEIN.

GN OSE705.

OS Oryza sativa (Rice).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; Liliopsida; Poales; Poaceae; Oryza.

OX NCBI_Taxid=4530;

RN [1]

RP SEQUENCE FROM N.A.

RC STRAIN-LONELLO;

RA Chen P.W., Chen L.J.;

RL Submitted (FEB-1998) to the EMBL/GenBank/DBJ databases.

DR EMBL; AF049348; AAD02494.1; -.

KM Hypothetical protein.

SO SEQUENCE 393 AA; 45258 MW; DBD01934BA2F9E95 CRC64;

Query Match 25.8%; Score 65; DB 10; Length 393;

Best Local Similarity 36.8%; Pred. No. 1.5;

Matches 14; Conservative 7; Mismatches 15; Indels 2; Gaps 1;

OY 5 ROYEBCRCQCM-QLETSQMRRCVSCDKRFEEDID 40

Db 37 KEELRMCKKCCRWEGAGDQRLRCEBCQLQROGEDDD 74

RESULT 9

ID 09SG14 PRELIMINARY; PRT; 554 AA.

AC 09SG14;

DT 01-MAY-2000 (TREMBlrel. 13, Created)

DT 01-MAY-2000 (TREMBlrel. 13, Last sequence update)

DT 01-OCT-2000 (TREMBlrel. 15, Last annotation update)

DE PUTATIVE GTPASE ACTIVATOR PROTEIN OF RAB-LIKE SMALL GTPASES (GTPASE

DE ACTIVATING-LIKE PROTEIN).

GN TG12.5 OR P2K15.210.

OS Arabidopsis thaliana (Mouse-ear cress).

OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;

OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;

OC Brassicales; Brassicaceae; Arabidopsis.

OX NCBI_Taxid=3702;

RN [1]

RP SEQUENCE FROM N.A.
 RC STRAIN-CV, COLUMBIA;
 RA Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.,
 RA Ranning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
 RA Bowman C.L., White O., Niernan W.C., Fraser C.M.;
 RT "Arabidopsis thaliana chromosome I BAC TIC12 genomic sequence.";
 RN Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 RL [1]
 RP SEQUENCE FROM N.A.
 RA Rieger M., Gabel C., Mueller-Auer S., Schaefer M., Zipp M.,
 RA Mewes H.W., Lemcke K., Mayer K.F.X., Queiler F., Salanoubat M.;
 RL Submitted (NOV-1999) to the EMBL/GenBank/DBJ databases.
 RN [1]
 RP SEQUENCE FROM N.A.
 RA EU Arabidopsis sequencing project;
 RL Submitted (JAN-2000) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AC012329; AAF16581.1; -;
 DR EMBL: AL132956; CAB66414.1; -;
 DR INTERPRO: IPR001195; -;
 DR PFAM: PF00566; TBC; 1;
 DR SQUENCE 554 AA; 63583 MW; 430BE1FCF1D8901C CRC64;

Query Match 25.4%; Score 64; DB 10; Length 554;
 Best Local Similarity 28.2%; Pred. No. 2.7;
 Matches 11; Conservative 10; Mismatches 18; Indels 0; Gaps 0;

QY 5 ROEYEECKRQCMOLETSGQMRRCVSCQCKRFEEDIDMSK 43
 DB 148 RKEYERLRQCKRLQKHNNGTRKLYNGSEITQDEYDMPR 186

RESULT 10
 Q9TTS4
 ID 09TTS4 PRELIMINARY; PRT; 564 AA.
 AC 09TTS4;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TEMBLrel. 14, Last annotation update)
 DE SCO-SPONDIN (FRAGMENT).
 GN SCO-SPONDIN.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 OX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-SUBCOMMISSURAL ORGAN;
 RA Gobron S., Creveaux I., Monnerie H., El Bitar F., Didier R.,
 RA Herbet A., Melniet R., Bamdad M., Dastugue B., Melniet A.;
 RT "Characterization of cattle SCO-spondin glycoprotein."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 DR EMBL: A1132107; CAB53760.1; -;
 DR INTERPRO: IPR001846; -;
 DR INTERPRO: IPR002919; -;
 DR PFAM: PF00094; vwd; 1.
 DR PFAM: PF01826; TIL; 2.
 FT NON_TER 1 564
 FT NON_TER 1 564
 SQ SEQUENCE 564 AA; 60337 MW; 2E22D4242F9BBE7C CRC64;

Query Match 25.0%; Score 63; DB 6; Length 564;
 Best Local Similarity 38.7%; Pred. No. 3.7;
 Matches 12; Conservative 6; Mismatches 9; Indels 4; Gaps 1;

QY 6 QEYEE-----CKRQCMOLETSGQMRRCVSCQCD 32
 DB 480 QEYQECAPACDRNGCEPDECGEIDNCVAGCN 510

RESULT 11

Q9SP11
 ID Q9SP11 PRELIMINARY; PRT; 489 AA.
 AC Q9SP11;
 DT 01-MAY-2000 (TEMBLrel. 13, Created)
 DT 01-MAY-2000 (TEMBLrel. 13, Last sequence update)
 DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
 DE SUCROSE BINDING PROTEIN HOMOLOG S-64.
 GN SBP.
 OS Glycine max (Soybean).
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I;
 OC Fabales; Fabaceae; Papilionoideae; Glycyne.
 OX NCBI_TaxID=3847;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Pedra J.H.F., Delu-Flilio N., Pirovani C.P., Contim L.S., Dewey R.E.,
 RA Oroni W.C., Fontes E.P.B.;
 RT "Antisense and sense expression of a sucrose binding protein homologue
 RT gene from soybean in transgenic tobacco affects plant growth and
 RT carbohydrate partitioning in leaves."
 RL Plant Sci. 0:0-0(1999).
 DR EMBL: AF191299; AAF05723.1; -;
 DR HSSP: P02853; 2PHL.
 DR INTERPRO: IPR001113; -;
 DR PFAM: PF00546; Seedstore_7s; 1.
 DR SQUENCE 489 AA; 55834 MW; 9BBC0D45EDCECD2 CRC64;

Query Match 24.8%; Score 62.5; DB 10; Length 489;
 Best Local Similarity 36.6%; Pred. No. 3.7;
 Matches 15; Conservative 3; Mismatches 14; Indels 9; Gaps 2;

QY 7 EYECKRQCMOLE--TSGQMRRCVSCQD-----KRFED 38
 DB 38 EIVTCKHQCGQGRYTESDKRTLCQCDMSKQREKVEEE 78

RESULT 12
 O60278
 ID 060278 PRELIMINARY; PRT; 875 AA.
 AC 060278;
 DT 01-AUG-1998 (TEMBLrel. 07, Created)
 DT 01-AUG-1998 (TEMBLrel. 07, Last sequence update)
 DT 01-OCT-2000 (TEMBLrel. 15, Last annotation update)
 DE KIAA0525 PROTEIN (FRAGMENT).
 GN KIAA0525.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BRAIN;
 RX MEDLINE=98280545; PubMed=9628581;
 RA Nagase T., Ishikawa K., Miyajima N., Tanaka A., Kotani H., Nomura N.,
 RA Ohara O.;
 RT "Prediction of the coding sequences of unidentified human genes. IX.
 RT The complete sequences of 100 new cDNA clones from brain which can
 RT code for large proteins in vitro."
 RL DNA Res. 5:31-39(1998).
 DR EMBL: AB011097; BAA25451.1; -;
 DR MEROPS: M01.018; -;
 DR INTERPRO: IPR00130; -;
 DR INTERPRO: IPR001930; -;
 DR PFAM: PF01433; Peptidase_M1; 1.
 DR PRINTS: PR00756; ALADIPRTASE.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 FT NON_TER 1 875
 FT NON_TER 1 875
 SQ SEQUENCE 875 AA; 99522 MW; C31A77DE516DEAFE CRC64;

Query Match 24.6%; Score 62; DB 4; Length 875;
 Best Local Similarity 37.8%; Pred. No. 7.6;

Matches 14: Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDKRPEEDIDW 41
 | | | | | : | | | | | : | | | |
 Db 812 RTRLEVKGFSSLKENGSQLRCVQOTITEENIGW 848

RESULT 13

Q9UKY2 PRELIMINARY; PRT; 941 AA.

AC Q9UKY2;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE ADIPOCYTE-DERIVED LEUCINE AMINOPEPTIDASE.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=9238715; PubMed=10220586;
 RA Hattori A., Matsumoto H., Mizutani S., Tsujimoto M.;
 RT "Molecular cloning of adipocyte-derived leucine aminopeptidase highly
 related to placental leucine aminopeptidase/oxytocinase.";
 RL J. Biochem. 125:931-938(1999).
 DR EMBL; AF106037; AAF07395.1; -;
 DR INTERPRO: IPR000130; -;
 DR INTERPRO: IPR001930; -;
 DR PFAM: PF01433; Peptidase_M1; 1.
 DR PRINTS: PR00756; ALADIPTASE.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Aminopeptidase.
 SQ SEQUENCE 941 AA; 107187 MW; 46BEF97CF78DEBC1 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;
 Best Local Similarity 37.8%; Pred. No. 8.1;
 Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDKRPEEDIDW 41
 | | | | | : | | | | | : | | | |
 Db 885 RTRLEVKGFSSLKENGSQLRCVQOTITEENIGW 921

RESULT 14

Q9UHF8 PRELIMINARY; PRT; 941 AA.

AC Q9UHF8;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
 DT 01-JUN-2000 (TrEMBLrel. 14, Last annotation update)
 DE AMINOPEPTIDASE PILS.
 GN APPILS.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Schomburg T.;
 RT "Molecular characterization of human aminopeptidase PILS.";
 RL Submitted (SEP-1999) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF183569; AAF20384.1; -;
 DR INTERPRO: IPR000130; -;
 DR INTERPRO: IPR001930; -;
 DR PFAM: PF01433; Peptidase_M1; 1.
 DR PRINTS: PR00756; ALADIPTASE.
 DR PROSITE: PS00142; ZINC_PROTEASE; UNKNOWN_1.
 KW Aminopeptidase.
 SQ SEQUENCE 941 AA; 107420 MW; 2ECA71F0BACBFD74 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;
 Best Local Similarity 37.8%; Pred. No. 8.1;
 Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDKRPEEDIDW 41
 | | | | | : | | | | | : | | | |
 Db 885 RTRLEVKGFSSLKENGSQLRCVQOTITEENIGW 921

RESULT 15

Q9NZ08 PRELIMINARY; PRT; 941 AA.

AC Q9NZ08;
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
 DE TYPE 1 TUMOR NECROSIS FACTOR RECEPTOR SHEDDING AMINOPEPTIDASE
 DE REGULATOR.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cui X., Alsady S., Lawrence M., Combs C.A., Rouhani F.N.,
 RA Levine S.J.;
 RT "Identification of an Aminopeptidase Regulator of Type I Tumor
 Necrosis Factor Receptor Shedding.";
 RL Submitted (JAN-2000) to the EMBL/Genbank/DBJ databases.
 DR EMBL; AF22340; AAF34664.1; -;
 DR RECEPTOR; Aminopeptidase.
 KW Receptor.
 SQ SEQUENCE 941 AA; 107234 MW; 22A0795C90155F04 CRC64;

Query Match 24.6%; Score 62; DB 4; Length 941;
 Best Local Similarity 37.8%; Pred. No. 8.1;
 Matches 14; Conservative 4; Mismatches 19; Indels 0; Gaps 0;

QY 5 ROYEBCRQCMOLETSGOMRCVSCDKRPEEDIDW 41
 | | | | | : | | | | | : | | | |
 Db 885 RTRLEVKGFSSLKENGSQLRCVQOTITEENIGW 921

Search completed: March 1, 2001, 16:08:59
 Job time: 1543 sec

